



08/984079

20 40  
CTT TCT ATT TGG TTA ACC ATG GCT CAT AAC TTT CGT CAT CCT TTC TTC  
Leu Ser Ile Trp Leu Thr Met Ala His Asn Phe Arg His Pro Phe Phe>  
60 80  
CTT TTC CAA CTT TTA CTC ATT ACT GTC TCA CTA ATG ATC GGT AGC CAC  
Leu Phe Gln Leu Leu Ile Thr Val Ser Leu Met Ile Gly Ser His>  
100 120 140  
ACC GTC TCG TCA GCG GCT CGA CAT TTA TTC CAC ACA CAA ACC ACC TCA  
Thr Val Ser Ser Ala Ala Arg His Leu Phe His Thr Gln Thr Thr Ser>  
160 180  
TCA GAG CTG CCA CAA TTG GCT TCA AAA TAC GAA AAG CAC GAA GAG TCT  
Ser Glu Leu Pro Gln Leu Ala Ser Lys Tyr Glu Lys His Glu Glu Ser>  
200 220 240  
GAA TAC AAA CAG CCA AAA TAT CAT GAA GAG TAC CCA AAA CAT GAG AAG  
Glu Tyr Lys Lys Gln Pro Lys Tyr His Glu Glu Tyr Pro Lys His Glu Lys>  
260 280  
CCT GAA ATG TAC AAG GAG GAA AAA CAA AAA CCC TGC AAA CAT CAT GAA  
Pro Glu Met Tyr Lys Glu Glu Lys Gln Lys Pro Cys Lys His His Glu>  
300 320  
GAG TAC CAC GAG TCA CGC GAA TCG AAG GAG CAC GAA GAG TAC GAT AAA  
Glu Tyr His Glu Ser Arg Glu Ser Lys Glu His Glu Glu Tyr Asp Lys>

FIGURE 1A



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340  
GAA AAA CCC GAT TTC CCC AAA TGG GAA AAG CCT AAA GAG CAC GAG AAA  
Glu Lys Pro Asp Phe Pro Lys Trp Glu Lys Pro Lys Glu His Glu Lys>  
360  
400  
CAC GAA GTC GAA TAT CCG AAA ATA CCC GAG TAC AAG GAG CAC AAA CAA GAT  
His Glu Val Glu Tyr Pro Lys Ile Pro Glu Tyr Lys Asp Lys Gln Asp>  
440  
GAG AAT AAG AAA CAT AAA GAT GAA GAG TGC CAG GAG TCA CAC GAA TCG  
Glu Asn Lys Lys His Lys Asp Glu Glu Cys Gln Glu Ser His Glu Ser>  
460  
500  
AAA GAG CAC GAA GAG TAC GAG AAA GAA AAA CCC GAT TTC CCC AAA TGG  
Lys Glu His Glu Glu Tyr Glu Lys Glu Lys Pro Asp Phe Pro Lys Trp>  
540  
GAA AAG CCT AAA GGG CAC GAG AAA CAT AAA GCC GAA TAT CCG AAA ATA  
Glu Lys Pro Lys Gly His Glu Lys Glu Lys His Lys Ala Glu Tyr Pro Lys Ile>  
560  
580  
CCT GAG TGC AAG GAA AAA CTA GAT GAG GAT AAG GAA CAT AAA CAT GAG  
Pro Glu Cys Lys Glu Lys Leu Asp Glu Asp Lys Glu His Lys His Glu>  
600  
620  
TTC CCA AAG CAT GAA AAA GAA GAG GAG AAG AAA CCT GAG AAA GGC ATA  
Phe Pro Lys His Glu Lys Glu Glu Lys Lys Pro Glu Lys Gly Ile>  
640  
660

FIGURE 1B



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680		700		720
GTA CCC TGA GTG GGT TAA AAT GCC TGA ATG GCC GAA GTC CAT GTT TAC		*		
Val Pro *** Val Gly *** Asn Ala *** Met Ala Glu Val His Val Tyr>				
	740		760	
TCA GTC TGG CTC GAG CAC TAA GCC TTA AGC CAT ATG ACA CTG GTG CAT				
Ser Val Trp Leu Glu His *** Ala Leu Ser His Met Thr Leu Val His>				
	780		800	
			*	
GTG CCA TCA TCA TGC AGT AAT TTC ATG GGA TAT TGT AAT TAT ATT GTT				
Val Pro Ser Ser Cys Ser Asn Phe Met Gly Tyr Cys Asn Tyr Ile Val>				
	820		840	860
AAT AAA AAA GAT GGT GAG TGG GAA ATG TGT GTG TGC ATT CAT CCA TGA				
Asn Lys Lys Asp Gly Glu Trp Glu Met Cys Val Cys Ile His Pro ***>				
	880		900	
			*	
GCA ATG CTG AAT CTC TTT GCA TGC ATA GAG ATT CTG AAT GGT TAT AGT				
Ala Met Leu Asn Leu Phe Ala Cys Ile Glu Ile Leu Asn Gly Tyr Ser>				
	920		940	960
TTA TGT TAT ATC GTT TGT TCT AGT GAA ATT AAT TTT GAA TGT TGT ATG				
Leu Cys Tyr Ile Val Cys Ser Ser Glu Ile Asn Phe Glu Cys Cys Met>				
TAA TGT T				
*** Cys Xxx>				

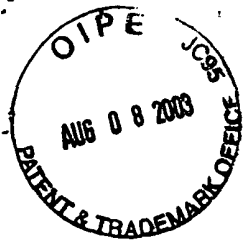
FIGURE 1C



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20 40 60  
ACTAAAGGGA ACAAAGCTG GAGCTCCACC GCGGTGGCGG CCGCTCTAGA ACTAGTGGAT  
80 100 120  
CCCCCGTGGA CTAACAACAAA CATGGGAAGA TTTGCTGTAA AAAAAATAAAA GAAGCTTACT  
140 160 180  
CAATAACACT TTGTGAATTG TATACAAAAG ACTCAATGAA AAACAATAAC TCAATACACT  
200 220 240  
TTTTTTCAC TATTACATC CTTTATATAG GCTGAAACTA CAACAACCTT AGCTAAAAAA  
260 280 300  
ATAGGATAAC CTAATAGCAA AATCACAATC AGATATTAAA CCATGATTTT AGCTAACCAT  
320 340 360  
TTAACAACTT TATTGAAACT AATTGAATA TTTTCATCTGC TGATATGCCC AAGATTTTAG  
380 400 420  
GCCACTAACC GATTGGTGG TGAACCTTAA CATGTCATGC ATTTGTAACT GTTTGAAACA  
440 460 480  
AGTTTTTTTGC ATTATTTTAC TATATGAACT GTTTGATTAG GTTGAGTTAC ACACTGAGCT  
500 520 540  
TGTAAGCTCA CTCAAAATTTT TCTAATTCTT AAGGTGATCA GCAAACTTAG GACCGGGCGG  
560 580 600  
CGTACGAGAG CTCGGATTGA TTTTCTAGTT AATAAATAAG ACGATTATG TTTTAACT

Figure 2A



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620	ATTATGGACT TTTTGGACTA TGTAAGTGT TGGGACTTTA TTTTGTGTTT TTATTTGCTT	640	660
680	TTTTTGGATT TAGTAATTAT TATTTTAAA CTGCAAAATT ATATGTTTTT ACAAACTAAG	700 *	720
740	TCACAGTTTT CAAAATTCCA TAACTTAGAA TTTTTCGCTG CAAAATAAAG TAATCATTTA	760	780
800 *	AGTGTTTTTT CTGTAATAAA ATAAATAAAT AATTTTAACG AGTATTTTCC TAAAAATTGG	820	840
860	AAATTGATTT ACCAAAATTA GTATGTCAAA ACACATGTTT ATATGTTACA GGGCGATATC	880	900 *
920	GTCTAGGCAA ATAACATCTA GCGGGGGTTT GGAGTGTAC AGGGCGAGTG GGCTCATTTT	940	960
980	GAGTAAGTAT AGTTAGGCC GAGTTTGA GAGTGTATTC AAGGTCAAAG ATTTTGTA	1000 *	1020
1040	CTTCGATGAA TGATATGTAT GATTGTCCGA TTAACGAAAT ATGTTTTTTT CTTTTGTGTG	1060	1080
1100 *	TGTTTTATCT CGTGTGATAA GTATATAGTA TGTTTTATTC CAATCTTAT GGCATGTGAC	1120	1140
1160	ATTGTGGCTA TTCTAATTAA ATTGATTGT TATTATTGAA ATCTGATGCA TCTGTCTTAC	1180	1200 *

Figur 2B



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1220	AAAGCATGGA ATCTCATGCC TACTGCTTTC TGTTAAAGAT ACGATTGCAA GTTTAACATG	1240	1260
1280	CTTACTATTT TGATTTTGTC CTTGCAATGCT ATGTCACATT ACATGGGGTT GGGATGATAT	1300 *	1320
1340	GGTAAGGAGG AAGTTTGGAC AGTTTAATGA TTTGCACTAT CTGGTGGTTT AACACATAT	1360	1380
1400 *	TTGTTATGGC ATCTTGACTG CGGTTATGGT GGCTCGACCG CCCATATCTG TTCTGGAAAT	1420	1440
1460	TTATCTGTGA CTCGTGGTGC ATTGTCTACA ATTATTTGTT GGTGTGTTTT GGATGGACGA	1480	1500 *
1520	GTCGTGGGA ACTCTATTG GTGTGTTGCG GAGTTGGGA GGAATTTTC GAAAAAAT	1540	1560
1580	TGCATTGTGT TTTTCTGAAA AATATTGCAT TAACATAATC ATGCATCTC AATTTTGGTC	1600 *	1620
1640	AATTGAACGT TATAAAATTC TCTATGATAT CCTGATCTGT TTATTACATT ATATGTGTTT	1660	1680
1700 *	ATGCTTGAGT TAAAGTCAAAC ATTGAGATTC ATAGCTCACC CAATTATTTA ATCATTTCAG	1720	1740
1760	GCAATCTGCA GACTTAGGAT TGGATGGCGT TCAGGAGCTT GGATTGGTTT TCTCACATCA	1780	1800 *
1820	TATTTTATTA AATAATTATT AATTAAAATT TATGGACTTT TGGACTGTCT GACTAAATTT	1840	1860

Figure 2C



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20 60  
ACTAAAGGGA ACAAAGCTG GAGCTCCACC GCGGTGGCGG CCGCTCTAGG ATCCCCCGTG  
80 120  
GACTAAACAA AACATGGGAA GATTGTCTGT AAAAAAATAA AAGAAGCTTA CTCAATAACA  
140 180  
CTTTGTGAAT TGTATACAAA AGACTCAATG AAAAAACAATA ACTCAATACA CTTTTTTTCA  
200 240  
CTGATTTACA TCCTTTATAT AGGCTGAAAC TACAACAACCT TTAGCTAAAA AAATAGGATA  
260 300  
ACCTAATAGC AAAATCACAA TCAGATATTA AACCATGATT TTAGCTAACC ATTTAAACAAC  
320 360  
TTTATTGAAA CTAATTTGAA TATTTCATCT GCTGATATGC CCAAGATTTT AGGCCACTAA  
380 420  
CCGATTGGT GGTGAACCTT AACATGTCTAT GCATTGTGTA CTGTTTGAAA CAAGTTTTT  
440 480  
GCATTATTTT ACTATATGAA CTGTTTGATT AGGTTGAGTT ACACACTGAG CTTGTAAGCT  
500 540  
CACTCAAATT TTTCTAATTT CTAAGGTGAT CAGCAAACCTT AGGACCGGGC GCGGTACGAG

Figure 3A



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560	AGCTCGGATT GATTTTCTAG TTAATAAATA AGACGATTTA TGTTTTAACTA CTATTATGGA	580	600 *
620	CTTTTGGAC TATGTAAC TG TTTGGGACTT TATTTTGTGTT TTTTATTGTC TTTTGTGGA	640	660
680	TTTAGTAATT ATTATTTTAA AACTGCAGAAA TTATATGTTT TTACAAACTA AGTCACAGTT	700 *	720
740	TTCAAAATTC CATAACTTAG AATTTTTCGC TGCAAAATAA AGTAATCATT TAAGTGTTTT	760	780
800 *	TTCTGTAATA AAATAAATAA ATAATTTTAA CGAGTATTTT CCTAAAAATT GGAAATTGAT	820	840
860	TTACCAAAAT TAGTATGTCA AAACACAATGT TTATATGTTA CAGGGCGATA TCGTCTAGGC	880	900 *
920	AAATAACATC TAGGCGGGT TTGGAGTGTT ACAGGGCGAG TGGGCTCATT TTGAGTAAGT	940	960
980	ATAGTTAGGG CCGAGTTTAA GATTGCATAT TCAAGGTCAA AGATTTTGTA AACTTCGATG	1000 *	1020
1040	AATGATATGT ATGATTGTCC GATTAACGAA ATATGTTTTT TTCTTTTGTG TGTGTTTTAT	1060	1080

Figur 3B





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1100	1110	1120	1140		
CTCGTGTGAT	AAGTATATAG	TATGTTTTAT	TCCAATTCTT	ATGGCATGTG	ACATTGTGGC
1160	1180	1200	*		
TATTCTAATT	AAATTGATTT	GTTATTATTG	AAATCTGATG	CATCTGTTCT	ACAAAAGCATG
1220	1240	1260			
GAATCTCATG	CCTACTGCTT	TCCTGTTAAAG	ATACGATTGC	AAGTTTAAACA	TGCTTACTAT
1280	1300	1320			
TTTGATTTTG	TCCTTGCATG	CTATGTCACA	TTACATGGGG	TTGGGATGAT	ATGGTAAGGA
1340	1360	1380			
GGAAGTTTIG	ACAGTTTAAAT	GATTGCACT	ATCTGGTGGT	TTAACCACAT	ATTGTGTTATG
1400	1420	1440			
GCATCTTGAC	TGCGGTTATG	GTGGCTCGAC	CGCCCATATC	TGTTCTGGAA	ATTATCTGT
1460	1480	1500	*		
GACTCTGGTG	GCATTGTCTA	CAATTATTG	TTGGTGTGTT	TTGGATGGAC	GAGTCGTGGG
1520	1540	1560			
GAACTCTATT	TGGTGTGTTG	CGGAGTTGGG	TAGGAAATTT	TCGAAAAAAA	TTTGCATTGT
1580	1600	1620	*		
GTTTTTCTGA	AAAATATTGC	ATTAACATAA	TCATGCATTC	TCAATTTTGG	TCAATTGAAC

Figure 3C



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1640	1660	1680
GTTATAAAAT TCTCTATGAT ATCCTGATCT GTTTATTACA TTATATGTGT TTATGCTTGA		
1700 *	1720	1740
GTAAAGTCAA ACATTGAGAT TCATAGCTCA CCCAATTATT TAATCATTTT AGGCAATCTG		
1760	1780	1800 *
CAGACTTAGG ATTGGAATGGC GTTCAGGAGC TTGGATTGGT TTCTCTCACAT CATATTTTAT		
1820	1840	1860
TAAATAAATTA TTAATTAAAA TTTATGGACT TTTGGACTGT CTGACTAATT TTCAGAAATTT		
1880	1900 *	1920
TATTTTGGTT TTGGGTTTGT TTGAATTTT TAGATAAATTA TTTTAAATAT TCTGCATAAT		
1940	1960	1980
TTTTCTGTTA TTTGAAAAGG ATGTTGGAAT TTTTTTTTCAA AATTGAAACG TTTAAGAATT		
2000 *	2020	2040
TTTACTACTG CAAATTCAGA ATAAGTGAAT TTGTTTTTTA GAAAGATTAA ATAAGTTAGT		
2060	2080	2100 *
ATTACGATTT TTAGTTTGAT TTGGTGGAAG GTAATGTATG TTTTGAACA TAATTATTG		
2120	2140	2160
ACAATAATTA AGTTTCTAG GGAATAACG GAAATATCTT CTCTTTTTT GTAAATAC		

Figure 3D



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2180	2200 *	2220
TAATGCAAGA ACAACAACG TTTTGGGGAG CAAATAATCT AGCTTTAAGT AGTCAGTGTA		
2240	2260	2280
ACTCTCAAAA TCTGGTCATA ACTTCTAGGC TGAGTTTGCT GTGCTACAGT AGTAAGTCTA		
2300 *	2320	2340
TAGAAACTTA CCTGACAAAA CGACATGACG TCAGGGTCGA ATCTACAACT TTTCCCTTTT		
2360	2380	2400 *
CTTCAATTAA CATATGGTTG ATTCAAGTTC CGATCTATAA TAATTATTATTA CGATTATATCA		
2420	2440	2460
ATTCAATTAA CCTTATATCA TCCTATTATA AATATAAGTC AGTTCAATTC AGTTTTCGAA		
2480	2500 *	2520
AGTTCCCCAA AATTTTGAAT TTTATTAAAT TTATTCCCTA AAACCGAAAT AGTTATACT		
2540	2560	2580
TTCAAATTTA AGTTTCATTT TTCAATCCGA TTTCAATTTC ATCCTTTTAT AACCTCTCTAT		
2600 *	2620	2640
TATCTATAAT TACATAAAAT TCAAATTAAT TTTGAAATAT TTACACTTTA GTCCCTAAGT		
2660	2680	2700 *
TCAAAACTAT AAATTTTCAC TTTAGAAATT AATCATTTTT CACATCTAAG CATCAAAATTT		

Figure 3E



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2720	2740	2760
AACCAAATGA CACAAATTTC ATGATTAGTT AGATCAAGCT TTTGAGTCTT CAAAACATAA		
2780	2800 *	2820
AAATTACAAA AAAAAACAA ACTTAAATC ATTTATCAAT TTGAACAACA AAGCTTGGCC		
2840	2860	2880
GAATGCTAAG AGCTTAAAAA TGGCTTCTTT TGTTCCTTTT TGTTGCAAC GGTGGAGAGA		
2900 *	2920	2940
AGAGGGAAT GAAGATTGAC CATATTTTTT TATTATGTTT TAACATATAA TATTAATAAT		
2960	2980	3000 *
TTAATCATAA TTATACTTTG GTGAATGTGA CAGTGGGAG ATACGTAAAG TATTTTAAAC		
3020	3040	3060
TTATACTTTT TGCAAGCAGT TGGCTGGTCT ACCCAAGAGT GATCAAAGTT TGAGCTGCCT		
3080	3100 *	3120
TCAATGAGCC AATTTTGGC CATAATGGAT AAAGGCAATT TGTTTAGTTC AACTGCTCAC		
3140	3160	3180
AGAATAATGT TAAATGAAA TTAAAAATAAG GTGGCCTGGT CACACACACA AAAAAAACT		
3200 *	3220	3240
AATGTTGGTT GGTGAATTT TATATTACGG AATGTAATAT TATATTTTAA AATAAAATTA		

Figure 3F



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3260	3280	3300 *
TGTTATTAG ATTCTTAATA TTTTGGAGCA TTCCATACTA TAATTTTCGTA ACATAATATT		
3320	3340	3360
AAAATATAGT AATATAAAGT GTAATTAACT TTAAATTACA AGCATAATAT TAAATTTTGA		
3380	3400 *	3420
ATCAATTAAT TTTTATTCT ATTATTTTAA TTAATTTAGT CTATTTTTC AAAATAAAAT		
3440	3460	3480
TTAAATCTAA ATAAAAATAA TTTTTCCTTA ATGTTGAAAC AACTCATGTT ATACTTCAAA		
3500 *	3520	3540
ATTATAAGTA TTATATTAC CTTGATGATT TATTTATTAG TATATTAATT CTGATTATAA		
3560	3580	3600 *
TTATGGTGG ATACAAATCGC TTTCCACTAA ATATTTTAACT TATGATTAT AAATTTATT		
3620	3640	3660
CAACATCGTA TATTTACTTA TTAATACATA ATTTATCATA ATTTTATGA AATTGAGACC		
3680	3700 *	3720
AAGAAACATT AAGAGAACA ATTCTATAAC AAAGACAATT TAGAAAAAA TGTACTTTTA		
3740	3760	3780
GGTAATTTTA AGTACTCTTA ACCAAACACA AAAATTCAAA TCAAATGAAC TAAATAAGAT		



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3800 \* 3820 3840  
AATATAACAT ACGGAACATC TTAAGTGTA TCTTACATTC CCATAATTTT ATTATGAAAA  
3860 3880 3900 \*  
ATAATCTTAT ATTACTCGAA CTAAGTGTTG TCACAAATTA TTATCTAAAT AAAGAAAAAC  
3920 3940 3960  
ACTTAATTTT TATAACATTT TTTTCATATAT TTGAAAGATT ATATTTTGTAT TATTACGTA  
3980 4000 \* 4020  
AAAAATATTG ACATAGATTG AGCACCTTCT TAACATAATC CCACCATAAG TCAAGTATGT  
4040 4060 4080  
AGATGAGAAA TTGGTACAAA CAACGTGGGG CCAATCCCA CCAAAACCATC TCTCATCTC  
4100 \* 4120  
TCCATATAAAA GGCTTGCTAC ACATAGACAA CAATCCACAC A CA AAT ACA CGT TCT  
4140 4160 4180  
TTT CTT TCT ATT TGA TTA ACC ATG G CTCATAGCAT TCGTCACCCCT TTCTTCCTTT  
<Lys Lys Arg Asn Ser \*\*\* Gly His  
<Ile Cys Thr Arg  
4200 \* 4220 4240  
TCCAACTTTT ACTCATAAGT GTCTCACTAG TGACCCGGTAG CCACACTGTT TCGGCAGCGG  
4260 4280 4300 \*  
CTCGACGTTT ATTCGAGACA CAAGCAACCT CATCAGAGCT CCCACAATTG GCTTCAAAAT

Figure 3H



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4320	ACGAAAAGCA	CGAAGAGTCT	GAATACGAAA	AGCCAGAATA	CAAAACAGCCA	AAGTATCACG
						4360
4380						
						4420
						4480
						4540
						4600
						4660
						4720
						4780
						4840
						4900
						4960
						5020
						5080
						5140
						5200
						5260
						5320
						5380
						5440
						5500
						5560
						5620
						5680
						5740
						5800
						5860
						5920
						5980
						6040
						6100
						6160
						6220
						6280
						6340
						6400
						6460
						6520
						6580
						6640
						6700
						6760
						6820
						6880
						6940
						7000
						7060
						7120
						7180
						7240
						7300
						7360
						7420
						7480
						7540
						7600
						7660
						7720
						7780
						7840
						7900
						7960
						8020
						8080
						8140
						8200
						8260
						8320
						8380
						8440
						8500
						8560
						8620
						8680
						8740
						8800
						8860
						8920
						8980
						9040
						9100
						9160
						9220
						9280
						9340
						9400
						9460
						9520
						9580
						9640
						9700
						9760
						9820
						9880
						9940
						10000

Figure 3I



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4920		4940	4960
TTACAAAGTTA	AGACATGTAT	AAATATATGA	CAATATAAAT ACAAGTTTTA GTTCAATGTT
4980		5000 *	5020
AGCTATCTTA	GATGTTTATT	GATGATCTTA	ATTACATTTA AACAAATTCC ACTTAAATTT
5040		5060	5080
TTAATAAATA	ATAACAAATA	ATTATTGTAA	TATAATACAT TAAATGCAAC AAAAAATGAA
5100 *		5120	5140
ATAAATAAAA	TAAATAGCA	AATAATTGTT	ATAATATTGT AATATAATAT GTACCATATT
5160		5180	5200 *
CTTAACTGAA	ATAGGGTCTA	ACCTATAATC	CCTAAAATTT CAGTTTAAAT ATTTTATATAC
5220		5240	5260
CTGCCATATT	ATTAGAACTC	TTTTTAAATA	TATTAAAATTT TTAATTATAC CAATTTAATT
5280		5300 *	5320
TAAACTATTA	ATTATCTTAA	CTAAAATCTA	AAATTTTATT TAACCTATTA ATTAAATTCC
5340		5360	5380
TAATTATCTT	ATCTAATTTA	AAACTCTAAT	TATCCCTAATT TGATTTAAAT TCTTGATTAT
5400 *		5420	5440
CTTAATTGTT	AACCTCCTCC	ACCCAGCTAG	ATGCTGGACC CGAATCCGGG AGATTACATC





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5460 5480 5500 \*  
GGCATTGAGA TGGCCTAGTA GTGATCAGGG TTTTCTAGAG GTACCCAATT CGCCCTATAG

TGAGTCGT



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AAAAAACA ATG AGC ACT GCA AGA TTT ATC AAG TGT GTC ACG GTC GGT GAT 50  
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp  
1 5 10

GGA GCT GTG GGG AAA ACT TGT ATG CTC ATT TCA TAT ACC AGC AAT ACT 98  
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr  
15 20 25 30

TTC CCA ACG GAT TAT GTT CCA ACA GTA TTT GAT AAC TTT AGT GCC AAT 146  
Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn  
35 40 45

GTG GTG GTG GAT GGC AGC ACA GTG AAC CTT GGC CTA TGG GAC ACT GCC 194  
Val Val Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala  
50 55 60

GGG CAA GAA GAT TAT AAT AGG CTA AGG CCA CTG AGT TAT AGA GGA GCT 242  
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala  
65 70 75

GAT GTG TTT TTG TTG GCC TTT TCT CTT ATA AGC AAG GCC AGT TAT GAA 290  
Asp Val Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu  
80 85 90

AAC ATC TAC AAA AAG TGG ATC CCA GAG CTA AGA CAT TAT GCT CAT AAT 338  
Asn Ile Tyr Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala His  
95 100 105 110

GTA CCA GTT GTG CTT GTT GGA ACC AAA CTA GAT TTG CGA GAT GAC AAG 386  
Val Pro Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Lys  
115 120 125

CAG TTC CTC ATT GAT CAC CCT GGA GCA ACA CCA ATA TCA ACA TCT CAG 434  
Gln Phe Leu Ile Asp His Pro Gly Ala Thr Pro Ile Ser Thr Ser Gln  
130 135 140

FIGURE 4A



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GGG GAA GAA CTA AAG AAG ATG ATA GGA GCA GTT ACT TAT ATA GAA TGC 482  
Gly Glu Glu Leu Lys Lys Met Ile Gly Ala Val Thr Tyr Ile Glu Cys  
145 150 155

AGC TCC AAA ACC CAA CAG AAT GTG AAG GCT GTT TTC GAT GCT GCA ATA 530  
Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile  
160 165 170

AAA GTA GCT TTG AGG CCA CCA AAA CCA AAG AGA AAG CCT TGC AAA AGG 578  
Lys Val Ala Leu Arg Pro Pro Lys Pro Lys Arg Lys Pro Cys Lys Arg  
175 180 185 190

AGA ACA TGT GCT TTC CTT TGAATATTGG ATCATTTATTA CAGTCAAAAA 626  
Arg Thr Cys Ala Phe Leu  
195

CAGTTAAACAA AAGCTGTGTC AGATAAACAC TGAATCTGCT ATAGTTTGTT TTTGGTTTAC 686

ATATGTTCCA CGTGAAACTA TGAAGCATCT CTAAGAAAAAC CCAAACTATC ATATCAACCC 746

ATCGATCAAT GAATCGATTT CAATTTTCGC AGTATAAGTT CCTTTTAATC CTTTCTTTTTT 806

ACTTCATTTT ATAACGAATT CTATGGATAA TGTTCCCTAC AAACATGTCA TTACAATGTT 866

TAATTATAAA TTCCATTCTT CTATTTTACT AAAAAAAAAA AAAA 910

FIGURE 4B



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20 40 60  
TTGGATGAGA ACCAATTTT AATAGTAAAN CCTAACCAAT TTTTAATAAT AAAGCTGACT  
80 100 120  
CCTAGTACAA GAGCTTTTAT TCATTCTTCT ATTTTGCTTT CCTCTAGGCT TGGCAATCGA  
140 160 180  
GAATTTTCTT GTGTACAAT ATAATAAATA CATCGTAGAA ATAAATTTTA TTCAAATTTGA  
200 220 240  
AGTCTTAACC ATCTTTAATA TTTGTAGATG TAATTTAAAT GAAAGATAAA TACATATTCT  
260 280 300  
TGGACATGTA TTTTCATCTT AATGTTTGTG GCTTTGGTGA TAGGTGTATT GATGTACGAT  
320 340 360  
GTCTTTTAA TACATATCA CATTITGAGT TTGTATGATG ATAAGTCGAC ATAANCGAAA  
380 400 420  
TATGGTGTGA TCTTCACITT TGAACITTGA TAAGTCACCA AACTTTAACA AAGTTTGATT  
440 460 480  
GTGTACATAT ATATATATAT CTTCAAAATTT TATAATAAAA ATTGTGTTTA AATAATTTAC  
500 520 540  
AGTTATATTA TTTTATATC TCTAATTTTA TTTGTGCGCA AATTTTGTAGT TGATATTTTA  
560 580 600  
ACATAAAAA AATTGTACAC ATTTACAAGC CCATATACAA ATAATTATAT AAATATTTCAT

FIGURE 5A



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TAAAAAATAT	ATTAAATAT	AGGATATAAA	TATAACTATT	TTAGAATTAT	TCTACTTTAA	620	640	660
GATAACATAG	GTAAATGTA	TAATTAATAA	GGTAGTTTA	TTGTAAAGAT	GAGTATATAT	680	700	720
GTGCTAAACA	TAATCACTAA	CCATTTTTAT	TAACTTCTTG	GTTTGTGAAGT	TCCAAAAAGA	740	760	780
AAATGGAAGG	GAAATTTGAG	AGTAAGTTCA	TGTTTATATT	ATACATAATG	AAGTTGATGT	800	820	840
TTTCTTCTTT	TTAATATTTT	TATACAAAAAT	ATTTAAATAA	AATAATTAAG	GATTGAATGA	860	880	900
AAAAATATAAT	GAAAGTCGTT	TTACTAATAG	TCATATTGCA	TTTTGTGCGCA	TCTACTTTAAA	920	940	960
TAATAGATAA	ATTAATTGTG	GTACATTAGA	TCAAAGAACA	AACTAGATTT	TGTCCCATTC	980	1000	1020
TATTGTTAAA	AGCTGGTCCG	TTTACATTAA	AATAAGGTAC	ATGTTACATG	CCACGTATAA	1040	1060	1080
CTATCTGGTT	ATTCTATCAA	TCACGCTAAT	TTTTAACAGT	AGAAATGAAT	GTAATTTTTTA	1100	1120	1140
AATAGAAAGG	GTCAAATTGT	TATTTGATCT	AACACGTAGG	GATTAAATTA	CTTATTTTCC	1160	1180	1200

FIGURE 5B



08/994099

1220 TAAAGAAATA AGTAAATAT AATTGAATC TTAATACAAA AACTTTCATG ATACTTTTAT 1260  
1280 CATATTTTAC TTATAATTTA ATATTGTGAG AGTAACAAAR TTAAAAAACA TAGAAACACC 1320  
1340 AAAAGTTAGT TATGGTGTGA CTCATATACA CAGTTAAAAAT TTGAATAAAT TTTTTCCTTC 1380  
1400 GTCATTAATT CCATCATGGG TTTTTTTTTT TCTAGTTAAG CCATAATTAT CAAAAATAATC 1440  
1460 ATCATTAATC CTATCAATAC CCGGCCCTGC CTCCCTCCCT CAATACTTAA ACCCAACTAA \* 1500  
1520 CACCCAGCAC CAAACGCACT TTAATAGCCA CCTATTCTA GCCATGTCCT TGCACCTTAAA 1560  
1580 GAAAAGTAAA GCTAACCTGC AATCATTTCCA TATCGAGGCC TCAACAGATA AAGTTGGTTG 1620  
1640 ATGGGTTTGC ACCAAGTTGT TAAAACCCGG CCTCAACTT CCTTTTCTT TTCAATCCTCC 1680  
1700 CCACTCCACA CCTTCCAATT TTCTTCATAT GGTTCATTA TAAGTTCTTT ATAATCACAG 1740  
1760 AATCAAGATA AGTCCTCAGC AAACAAAAA CCATGGCTCT CGAGCAAGAT CTGGACTAGT \* 1800

FIGURE 5C



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1820	1840	1860
CAGAGCTCTG AATATTGGAT CATTATTACA GTCAAAAACA GTTAACAAAA GCTGTTGCAG		
1880	1900	1920
ATAAACACTG AATCTGCTAT AGTTTGTTTT TGGTTTACAT ATGTTCCACG TGAAACTATG	*	
1940	1960	1980
AAGCATCTCT AAGAAAACCC AAACATATCAT ATCAACCCAT CGATCAATGA ATCGATTTC		
2000	2020	2040
ATTTTCGCAG TATAAGTTCC TTTTAATCCT TTCTTTTTTAC TTCATTTTAT AACGAATTCT		
2060	2080	2100
ATGGATAATG TTCCCTACAA ACATGTCATT ACAATGTTTA ATTATAAATT CCATTCTTCT		*
2120	2140	2160
ATTTTACTAA GATATTAGTA ACTTCAAACT GCTGATTTTT ACTAATTTAT TATTATATAA		
2180	2200	2220
TTGTTAGAAT GATTATTTTT CAATAATTTA ACAACAATAT TTAATATTAT TATTATTATT	*	
2240	2260	2280
ATTTCTCAAT TTTTATTAAA CAAAAACATA AATTTTIGAC AAATTAATAA AAATGAATTA		
2300	2320	2340
ATTTCTCAAT TTTTCGTGCA ACTATTACAA AAATCCTTCA TAGTCCTAAT CTTAATTTGA	*	
2360	2380	2400
TGCAGAGGTG ATAATAATCT TAATTGATG CAGAGGTAAT AATGGGCCGG GTTTGAGCTG		*

FIGURE 5D

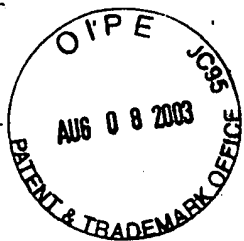


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2420	2440	2460
GACTTAAGCA TGATATTGAC GTACTTTTATA TTTTTCCTAAA TTCAACCCAG CTCGAAATAT		
2480	2500 *	2520
GAGTCTAAAA TTTTGTCCAA TTAAATCCAA GCCCAATTTA AGTTCGTCCA TATTATTTTT		
2540	2560	2580
TAATTTAAAA AATTATATC ATTTTATTTT AATATTTAAT TATTTTATAT ATTTTATTAT		
2600 *	2620	2640
TATTGAAAAAT TTTTATATAG TCATCTTAAC ATTATGTTAA TGTTTATATT AGAGTAGTAT		
2660	2680	2700 *
TATATATATT TAGTATAGGT TTATTTTGGT AATAAACTTA AAAATGGGTC TTGTGGGCTA		
2720	2740	2760
GACTTGGACC TTAAATGCTC AAACTCAAAC TTAAATTCATA TTTTAAACAG GCTTAATATT		
2780	2800 *	2820
TTTATTTTACA CTGTTTCAA TTTTTCGGGT GAAATATCTT CGAGTCTAGA TTAATAACAC		
2840	2860	2880
CACAGGTCTA ATTTGATGCT CAATGAAAAAT GAAATCATAT TGAGCTTAAT TAATATTCCA		
2900 *	2920	2940
TTCTTCTTTG CTGAAAGGAC CAAGCAATTC GAGTTACATT AAGGTTAAAG AGTATGGGAT		
2960	2980	3000 *
CCGCCAAACC TGCCCCAATG TCTCTTCAAC CATCCAAAAA CTTGAGTCAG TATCACATAC		

FIGURE 5E





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3020 ATGTACCGNT ATTTATTTAT TTATTGAAAT TGGCATTATT TCTTG  
3040

FIGURE 5F



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GGGCATTCCA CAGGACCATG TGTCCTCCCTAT TTCCAGGCAT TTTGAGACTT CACCTAAACT 60  
TCTAGAGTTG TTTCAAATTA GCCCCTATTT GTTCTTAAAT CATTTTAGGA TCTTGTAAC 120  
TCGTATTTAG GACTAAATGT GTAATTATA CTTTAATTAT GATTGATTAA TTGATTGATT 180  
TNGTAGTAAT GCCCGTGACC CTAATCCGTT AGCGAAGAGG GGTAGGGGT TAGGGGTTTT 240  
ATTATTATTT TTTAGATATT GTATAACTCT TGTTTTATTT TTAATTTTGT TACTATTTCA 300  
AAGGCATTTG TTTGTAGTGT TATTTTCGAGT AGGTTTTATG GGTGAACAAC CCTTGACCCG 360  
CAAATCAATC ACAAGAGTTC AACATTTTAT TTATTTTGAA ATGTATTAAA AATCGTTAAT 420  
CTATATATTC GCCCCATTAT TGGGATTAAA TATTCACAAG GGTTAGACC GTCATGAGAC 480  
AGATTAGTTT TATCTTACTG ATGGTCACAT CACAATAGTA ATTCAACTTA ATACGAGAGG 540  
AACCATTGAT TCACGCAATT GGTCAATCGCA CTTAGTTGAA AAGCTAGGGG TCGGAAGCTA 600  
CCGTACGCTG GATTATGATT GAACACCTCT AAGTCAGAAAT CCGAATTAGA AACAAATGCAC 660  
GTGTCCGTTG CCTGATTGCC AACCCCAATA ACACGTGTTG TAGGTTTAAAC CATGTTTATG 720  
AAAGATAAGG TTTTTTTTTT TATAAGCAAG CAACTATAGG GGTTTACTTC CGTGCGCAA 780  
TTTTTTAGGT ACCTATTTTG GGAGGGGGGA TTATGATTCA AGTGAAGAA AGTTGGCACA 840  
CACACAATCA GTACATCTGT TTTGACAGAG ACACAGCCTA AAAACAGCAG CAAACAAGCC 900  
TAAAGGAATC ACCCAAAAAC AACAAACAAA AGTACAGAGG AAAACAAGA AATCCCTGTT 960  
ACCACCAAGC TGAATAAAAG AAAATAAAAC TCAACTTTTG GCAATAAAA CCCCTCTACC 1020  
CTCAACCCCT AACCAACGCA CAATCAGCAA TACTCCAAGC AACCATTTTC CTTACAAGTT 1080

FIGURE 7A



08/994 099

TGTTTTTCTT GTGATTAAATC CAT ATG GCT AGC TCC ATG TCC CTT AAG CTT GCA 1133  
Met Ala Ser Ser Met Ser Leu Lys Leu Ala>  
  
TGT CTG CTA GTG TTG TGC ATG GTG GTG GGT GCA CCC CTG GCT CAA GGG 1181  
Cys Leu Leu Val Leu Cys Met Val Val Gly Ala Pro Leu Ala Gln Gly>  
  
GAC GTA ACC CGT GCT GAT GGC GTA GTC ACC CTT CCA CGC TGC CTT CCT 1229  
Asp Val Thr Arg Ala Asp Gly Val Val Thr Leu Pro Arg Cys Leu Pro>  
  
TTA TTG ATA GGG AAT GGT AAT GGT GCT GAT GCT GAT GAT GCC CCA 1277  
Leu Leu Ile Gly Asn Gly Asn Gly Ala Asp Val Asp Ala Pro>  
  
GCT TGC TGC GAC ATC AGG GGT CTC TTG AGC TCG CTG CTC TGT GGT 1325  
Ala Cys Cys Asp Ile Val Arg Gly Leu Leu Ser Ser Leu Cys Gly>  
  
GGT GTT TAGGAACCG ATCTAGCTTG AAATCGGGTT CGGATACGGG TGGAGTTTCA 1380  
Gly Val>  
  
AATTGGTGTG TTATGGAATC CCAACTTAAT CGTGTTTAGG GGTGGGATCC AATTGTGTGA 1440  
TACATTACAG AGCATGGTTG TGGATTGTTT TCTCATATGT TTTGATTGAC TTGCTTGATA 1500  
CATTGGATGA TTCGATAAGG TGACCGGTTT ACCTGGGTAT CCAACCATCA TCCGATTACT 1560  
TTTTAATAAT TATTTGTTTC TTCTTTATGT TGTCTGTCTT TTTGTTTCTT GATCTATAAC 1620  
ATTATATTG CCCAAATTTT CGCATTITTCC ATATGTAGCT TATATATGTA TATATATATT 1680  
CAATAAAGTA TATTGATTTA GCAGATGATT TGTGTATATA TTAAATCAA ATCAAACATT 1740  
AATGATCATT CACTAGCGTC TTAATCTTGA AAAATTCAATC AACGGTTATC CTTTGCAGCA 1800  
TATATAAAAA AAATTGCCAA CCCTATGCTT TTACACCTAA TTCAAGGGAT AACATAAGTC 1860  
GATTAAACG A 1871

FIGURE 7B



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Coker 130	Yxy, Y	Yxy, x	Yxy, Y	Lab, L	Lab, a	Lab, b	LCh, L	LCh, C	LCh, h
1	80.35	.3206	0.3266	91.84	0.16	5.51	91.84	5.51	88.4
2	77.62	.3232	0.3282	90.6	0.66	6.45	90.6	6.48	84.2
3	80.98	.3197	0.3257	92.12	0.13	5.04	92.12	5.04	88.6
4	80.16	.3200	0.3255	91.75	0.35	5.00	91.75	5.01	86.1
5	77.03	.3220	0.3271	90.33	0.61	5.84	90.33	5.87	84.1
6	73.67	.3258	0.3293	88.76	1.35	7.14	88.76	7.26	79.4
7	82.43	.3178	0.3237	92.76	0.15	4.05	92.76	4.05	87.9
8	82.21	.3196	0.3255	92.66	0.19	4.99	92.66	4.99	87.9
9	81.19	.3194	0.3241	92.21	0.77	4.42	92.21	4.48	80.2
10	76.11	.3243	0.329	89.9	0.74	6.89	89.9	6.92	84
11	82.28	.3178	0.3236	92.69	0.19	4.00	92.69	4.00	87.3
TOTAL	874.03	3.5302	3.5883	1005.62	5.30	59.33	1005.62	59.61	938.10
MEAN	79.46	.3209	.3262	91.42	0.48	5.39	91.42	5.42	85.28
S.D.	2.91	.0026	.0020	1.33	0.38	1.08	1.33	1.11	3.22
RANGE	82.43-73.67	.3858-.3178	0.3293-.3236	92.76-88.76	1.35-.13	7.14-4.00	92.76-88.76	7.26-4.00	88.6-79.4
AVER DEV	2.44	.0021	.0017	1.11	0.31	0.88	1.11	0.90	2.64
Coker 130	Hunter L	Hunter a	Hunter B						
1	89.63	0.15	5.42						
2	88.10	0.66	6.27						
3	89.98	0.13	4.98						
4	89.53	0.36	4.94						
5	87.76	0.61	5.69						
6	85.83	1.35	6.85						
7	90.79	0.15	4.03						
8	90.67	0.19	4.95						
9	90.10	0.78	4.38						
10	87.23	0.75	6.65						
11	90.70	0.19	3.98						
TOTAL	980.32	5.32	58.14						
MEAN	89.12	0.48	5.29						
S.D.	1.65	0.39	0.99						
RANGE	90.79-85.83	1.35-.13	6.85-3.98						
AVER DEV	1.37	0.31	0.81						

FIGURE 9

FIGURE 10



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5149	Yxy, Y	Yxy, x	Yxy, Y	Lab, L	Lab, a	Lab, b	LCh, L	LCh, C	LCh, h
68-1	65.75	0.3351	0.34	84.86	0.72	11.9	84.86	11.92	86.6
68-1	62.54	0.3458	0.3474	83.19	2.14	15.84	83.19	15.98	82.4
68-1	62.56	0.3458	0.3474	83.2	2.14	15.85	83.2	15.99	82.4
8-1	84.72	0.3196	0.3278	93.76	0.89	5.87	93.76	5.93	98.6
68-1	64.97	0.3316	0.3354	84.46	1.17	9.81	84.46	9.87	83.3
17-2	64.42	0.3423	0.3436	84.18	2.26	14.19	84.18	14.36	81
17-3	60.97	0.3475	0.3475	82.36	2.74	16.03	82.36	16.26	80.4
17-15-1	64.02	0.3433	0.3444	83.97	2.34	14.57	83.97	14.75	80.9
21-1	59.32	0.3443	0.3445	81.46	2.64	14.41	81.46	14.64	79.7
21-3	63.64	0.34	0.3409	83.77	2.4	12.89	83.77	13.11	79.5
21-6	67.12	0.3372	0.3394	85.56	1.88	12.15	85.56	12.29	81.3
50-3-1	61.26	0.3502	0.3511	82.51	2.4	17.63	82.51	17.79	82.3
67-1	64.34	0.3434	0.3442	84.13	2.48	14.58	84.13	14.78	80.4
68-1	64.12	0.3442	0.3447	84.02	2.58	14.85	84.02	15.07	80.2
68-2	70.21	0.3428	0.3447	87.09	2.05	15.04	87.09	15.17	82.3
68-3	63.81	0.3457	0.3468	83.86	2.35	15.76	83.86	15.93	81.6
5149	Hunter L	Hunter a	Hunter B						
68-1	81.08	0.71	10.89						
68-1	79.08	2.08	14						
68-1	79.09	2.09	14.02						
8-1	92.04	0.91	5.81						
68-1	80.6	1.15	9.06						
17-2	80.25	2.21	12.75						
17-3	78.08	2.68	14.09						
17-15-1	80.01	2.29	13.05						
21-1	77.01	2.56	12.73						
21-3	79.77	2.35	11.65						
21-6	81.92	1.86	11.14						
50-3-1	78.26	2.33	15.36						
67-1	80.2	2.43	13.07						
68-1	80.07	2.53	13.28						
68-2	83.79	2.04	13.68						
68-3	79.87	2.3	14						

FIGURE 11



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5616	Yxy, Y	Yxy, x	Yxy, Y	Lab, L	Lab, a	Lab, b	LCh, L	LCh, C	LCh, h
11-1	72.26	0.3215	0.3254	88.09	1.1	5.06	88.09	5.17	77.8
11-2	58.69	0.3284	0.3335	81.12	0.6	8.36	81.12	8.38	85.9
11-2	52.78	0.3358	0.3335	77.74	3.55	9.22	77.74	9.87	69
11-1	72.03	0.3312	0.3338	87.98	1.72	9.52	87.98	9.67	79.8
11-1	72.34	0.3295	0.332	88.13	1.79	8.64	88.13	8.82	78.4
11-1	71.98	0.3295	0.3313	87.95	2.09	8.39	87.95	8.64	76.1
11-1	73.01	0.3256	0.3305	88.45	0.68	7.51	88.45	7.54	84.9
17-1-2	75.85	0.3274	0.3306	89.78	1.52	7.94	89.78	8.08	79.3
17-3-1	72.6	0.3271	0.3303	88.25	1.48	7.66	88.25	7.8	79.1
17-4-1	69.02	0.3352	0.3377	86.51	1.78	11.37	86.51	11.5	81.2
25-11-1	69.5	0.3364	0.3401	86.75	1.26	12.41	86.75	12.47	84.2
25-28-1	72.21	0.3324	0.3343	88.06	2.09	9.9	88.06	10.11	78.2
25-36-2	70.46	0.3327	0.3353	87.22	1.73	10.22	87.22	10.36	80.5
35-35-1	75.59	0.3268	0.3299	89.66	1.56	7.58	89.66	7.73	78.4
50-12-1	73.13	0.3284	0.3316	88.5	1.46	8.36	88.5	8.48	80.1
KS-11-2	65.33	0.3371	0.3388	84.65	2.07	11.83	84.65	12	80.1
5616	Hunter L	Hunter a	Hunter B						
11-1	85	1.09	4.89						
11-2	76.61	0.58	7.64						
11-2	72.64	3.38	8.22						
11-1	84.87	1.72	8.97						
11-1	85.05	1.79	8.2						
11-1	84.84	2.08	7.96						
11-1	85.44	0.67	7.18						
17-1-2	87.08	1.52	7.62						
17-3-1	85.2	1.48	7.31						
17-4-1	83.07	1.76	10.52						
25-11-1	83.36	1.25	11.43						
25-28-1	84.97	2.08	9.32						
25-36-2	83.94	1.72	9.56						
35-35-1	86.94	1.57	7.29						
50-12-1	85.51	1.46	7.96						
KS-11-2	80.82	2.04	10.81						

FIGURE 12

[illegible]